

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/080,354B

AU 1812

DATE: 04/13/94  
TIME: 17:04:18

INPUT SET: S1962.raw

This Raw Listing contains only the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

## (1) General Information:

- (i) APPLICANT: Breece, Tim  
Hayenga, Kirk  
Rinderknecht, Ernst  
Vandlen, Richard  
Yansura, Daniel

(ii) TITLE OF INVENTION: PROCESS FOR PRODUCING RELAXIN

(iii) NUMBER OF SEQUENCES: 40

## (iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Mr. Walter H. Dreger  
(B) STREET: 4 Embarcadero Center, Suite 3400  
(C) CITY: San Francisco  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 94111

## (v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

## (vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/080,354  
(B) FILING DATE: 21-JUN-1993  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Dreger, Walter H.  
(B) REGISTRATION NUMBER: 24,190  
(C) REFERENCE/DOCKET NUMBER: A-58117/WH

## (ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (415) 781-1989  
(B) TELEFAX: (415) 398-3249

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

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RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/080,354BDATE: 04/13/94  
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47 (A) LENGTH: 11 amino acids  
48 (B) TYPE: amino acid  
49 (C) STRANDEDNESS: single  
50 (D) TOPOLOGY: linear  
51  
52 (ii) MOLECULE TYPE: peptide  
53  
54 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
55  
56 Met Lys Lys Asn Ile Ala Phe Leu Leu Lys Arg  
57 1 5 10  
58  
59  
60 (2) INFORMATION FOR SEQ ID NO:2:  
61  
62 (i) SEQUENCE CHARACTERISTICS:  
63 (A) LENGTH: 29 amino acids  
64 (B) TYPE: amino acid  
65 (C) STRANDEDNESS: single  
66 (D) TOPOLOGY: linear  
67  
68 (ii) MOLECULE TYPE: peptide  
69  
70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
71  
72 Asp Ser Trp Met Glu Glu Val Ile Lys Leu Cys Gly Arg Glu Leu Val  
73 1 5 10 15  
74  
75 Arg Ala Gln Ile Ala Ile Cys Gly Met Ser Thr Trp Ser  
76 20 25  
77  
78  
79 (2) INFORMATION FOR SEQ ID NO:3:  
80  
81 (i) SEQUENCE CHARACTERISTICS:  
82 (A) LENGTH: 13 amino acids  
83 (B) TYPE: amino acid  
84 (C) STRANDEDNESS: single  
85 (D) TOPOLOGY: linear  
86  
87 (ii) MOLECULE TYPE: peptide  
88  
89 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
90  
91 Lys Arg Lys Pro Thr Gly Tyr Gly Ser Arg Lys Lys Arg  
92 1 5 10  
93  
94  
95 (2) INFORMATION FOR SEQ ID NO:4:  
96  
97 (i) SEQUENCE CHARACTERISTICS:  
98 (A) LENGTH: 24 amino acids  
99 (B) TYPE: amino acid

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100 (C) STRANDEDNESS: single  
101 (D) TOPOLOGY: linear  
102  
103 (ii) MOLECULE TYPE: peptide  
104  
105 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
106  
107 Gln Leu Tyr Ser Ala Leu Ala Asn Lys Cys Cys His Val Gly Cys Thr  
108 1 5 10 15  
109  
110 Lys Arg Ser Leu Ala Arg Phe Cys  
111 20  
112  
113  
114 (2) INFORMATION FOR SEQ ID NO:5:  
115  
116 (i) SEQUENCE CHARACTERISTICS:  
117 (A) LENGTH: 13 amino acids  
118 (B) TYPE: amino acid  
119 (C) STRANDEDNESS: single  
120 (D) TOPOLOGY: linear  
121  
122 (ii) MOLECULE TYPE: peptide  
123  
124 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  
125  
126 Lys Arg Lys Pro Thr Gly Tyr Gly Ser Arg Lys Lys Arg  
127 1 5 10  
128  
129  
130 (2) INFORMATION FOR SEQ ID NO:6:  
131  
132 (i) SEQUENCE CHARACTERISTICS:  
133 (A) LENGTH: 13 amino acids  
134 (B) TYPE: amino acid  
135 (C) STRANDEDNESS: single  
136 (D) TOPOLOGY: linear  
137  
138 (ii) MOLECULE TYPE: peptide  
139  
140 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  
141  
142 Asp Lys Lys Arg Thr Gly Tyr Gly Ser Arg Arg Arg Lys  
143 1 5 10  
144  
145  
146 (2) INFORMATION FOR SEQ ID NO:7:  
147  
148 (i) SEQUENCE CHARACTERISTICS:  
149 (A) LENGTH: 13 amino acids  
150 (B) TYPE: amino acid  
151 (C) STRANDEDNESS: single  
152 (D) TOPOLOGY: linear

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153
154      (ii) MOLECULE TYPE: peptide
155
156      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
157
158      Asp Lys Lys Arg Thr Gly Tyr Gly Ser Arg Lys Lys Arg
159          1             5             10
160
161
162      (2) INFORMATION FOR SEQ ID NO:8:
163
164          (i) SEQUENCE CHARACTERISTICS:
165              (A) LENGTH: 13 amino acids
166              (B) TYPE: amino acid
167              (C) STRANDEDNESS: single
168              (D) TOPOLOGY: linear
169
170          (ii) MOLECULE TYPE: peptide
171
172          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
173
174          Lys Arg Lys Pro Thr Gly Tyr Gly Ser Arg Arg Arg Lys
175              1             5             10
176
177
178      (2) INFORMATION FOR SEQ ID NO:9:
179
180          (i) SEQUENCE CHARACTERISTICS:
181              (A) LENGTH: 231 base pairs
182              (B) TYPE: nucleic acid
183              (C) STRANDEDNESS: single
184              (D) TOPOLOGY: linear
185
186          (ii) MOLECULE TYPE: cDNA
187
188          (ix) FEATURE:
189              (A) NAME/KEY: CDS
190              (B) LOCATION: 1..231
191
192          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
193
194      ATG AAA AAG AAT ATC GCA TTT CTT CTT AAA CGG GAC TCA TGG ATG GAG      48
195      Met Lys Lys Asn Ile Ala Phe Leu Leu Lys Arg Asp Ser Trp Met Glu
196          1             5             10             15
197
198      GAA GTT ATT AAA TTA TGC GGC CGC GAA TTA GTT CGC GCG CAG ATT GCC      96
199      Glu Val Ile Lys Leu Cys Gly Arg Glu Leu Val Arg Ala Gln Ile Ala
200              20             25             30
201
202      ATT TGC GGC ATG AGC ACC TGG AGC AAA AGG AAA CCC ACT GGT TAT GGT      144
203      Ile Cys Gly Met Ser Thr Trp Ser Lys Arg Lys Pro Thr Gly Tyr Gly
204              35             40             45
205

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206 TCT CGA AAA AAG AGA CAA CTC TAC AGT GCA TTG GCT AAT AAA TGT TGC      192
207 Ser Arg Lys Lys Arg Gln Leu Tyr Ser Ala Leu Ala Asn Lys Cys Cys
208      50                      55                      60
209
210 CAT GTT GGT TGT ACC AAA AGA TCT CTT GCT AGA TTT TGC      231
211 His Val Gly Cys Thr Lys Arg Ser Leu Ala Arg Phe Cys
212      65                      70                      75
213
214
215 (2) INFORMATION FOR SEQ ID NO:10:
216
217 (i) SEQUENCE CHARACTERISTICS:
218 (A) LENGTH: 593 base pairs
219 (B) TYPE: nucleic acid
220 (C) STRANDEDNESS: single
221 (D) TOPOLOGY: linear
222
223 (ii) MOLECULE TYPE: cDNA
224
225 (ix) FEATURE:
226 (A) NAME/KEY: CDS
227 (B) LOCATION: 431..586
228
229 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
230
231 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA      60
232
233 GTTGTATTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAA GAACTGTGTG CGCAGGTAGA      120
234
235 AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG      180
236
237 GTTGATTGAT CAGGTAGAGG GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCTCTGA      240
238
239 CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA      300
240
241 AAAAGTTAAT CTTTTCAACA GCTGTCATAA AGTTGTCACG GCCGAGACTT ATAGTCGCTT      360
242
243 TGTTTTTTATT TTTTAATGTA TTTGTACGCA AGTTCACGTA AAAAGGGTAT CTAGAGGTTG      420
244
245 AGGTGATTTT ATG AAA AAG AAT ATC GCA TTT CTT CTT GCA TCT ATG TTC      469
246 Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe
247      1                      5                      10
248
249 GTT TTT TCT ATT GCT ACA AAT GCC TAT GCA GAC TCA TGG ATG GAG GAA      517
250 Val Phe Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ser Trp Met Glu Glu
251      15                      20                      25
252
253 GTT ATT AAA TTA TGC GGC CGC GAA TTG GTA CGC GCG CAA ATA GCG ATA      565
254 Val Ile Lys Leu Cys Gly Arg Glu Leu Val Arg Ala Gln Ile Ala Ile
255      30                      35                      40                      45
256
257 TGC GGT ATG AGT ACA TGG AGT TGAAGAA      593
258 Cys Gly Met Ser Thr Trp Ser

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/08/080,354B**

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Original Text